

OIKE

RAW SEQUENCE LISTING

DATE: 08/16/2001

PATENT APPLICATION: US/09/924,946

TIME: 12:48:57

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\08162001\I924946.raw

4 <110> APPLICANT: American Home Products Corporation
 5 Evans, Mark
 6 Scicchitano, Marshall
 7 Bapat, Ashok
 8 Beer, Eric
 9 Bhat, Ramesh
 10 Ferris, Elissa
 11 Mastroeni, Rob
 12 Zhang, Jianxiong
 13 Karathanasis, Sotirios K.
 15 <120> TITLE OF INVENTION: A Novel Member of the Lysyl Oxidase Gene Family
 17 <130> FILE REFERENCE: 0630/1G703-US2
 19 <140> CURRENT APPLICATION NUMBER: US/09/924,946
 20 <141> CURRENT FILING DATE: 2001-08-08
 22 <150> PRIOR APPLICATION NUMBER: 60/223,763
 23 <151> PRIOR FILING DATE: 2000-08-08
 25 <150> PRIOR APPLICATION NUMBER: 60/255,838
 26 <151> PRIOR FILING DATE: 2000-12-15
 28 <160> NUMBER OF SEQ ID NOS: 11
 30 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 3616
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Human
 37 <400> SEQUENCE: 1

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40	tggcgtggtc	cccaccagcc	accctctttc	tgttctgtct	gctgctaggc	cagccccctc	180
41	ccagcaggcc	acagtcactg	ggcaccacta	agctccggct	ggtgggcccc	gagagcaagc	240
42	cagaggaggg	cgccctggag	gtgctgcacc	agggccagtg	gggcaccgtg	tgtgatgaca	300
43	actttgctat	ccaggaggcc	acagtggctt	gccgccagct	gggcttcgaa	gctgccttga	360
44	cctgggcccc	cagtgcacaag	tacggccaag	gggagggacc	catctggctg	gacaatgtgc	420
45	gctgtgtggg	cacagagagc	tccttggaac	agtgcgggtc	taatggctgg	ggagtcagtg	480
46	actgcagtea	ctcagaagac	gtaggggtga	tatgccaccc	ccggcgccat	cgtggctacc	540
47	tttctgaaac	tgtctccaat	gcccttgggc	cccaggggcg	gcggctggag	gaggtgcggc	600
48	tcaagcccat	ccttgccagt	gccaagcagc	atagcccagt	gaccgaggga	gccgtggagg	660
49	tgaagtatga	gggccactgg	cggcagggtg	gtgaccaggg	ctggaccatg	aacaacagca	720
50	gggtggtgtg	cgggatgctg	ggcttcccc	gcgaggtgcc	tgtcgacagc	cactactaca	780
51	ggaaagtctg	ggatctgaag	atgagggacc	ctaagtctag	gctgaagagc	ctgacgaata	840
52	agaactcctt	ctggatccac	caggtcacct	gcctggggac	agagccccac	atggccaact	900
53	gccaggtgca	ggtggctcca	gcccggggca	agctgcggcc	agcctgcccc	ggtggcatgc	960
54	atgctgtggg	cagctgtgtg	gcaggggctc	acttcggccc	accgaagaca	aagccacaac	1020
55	gcaaagggtc	ctgggcagag	gagccgaggg	tgcgctgcg	ctccggggcc	caggtggggc	1080
56	agggccgggt	ggaagtgtc	atgaaccgcc	agtggggcac	ggtctgtgac	cacaggtgga	1140
57	acctcatctc	tgccagtgtc	gtgtgtctgc	agctgggctt	tggtctgtct	cgggagggcc	1200
58	tctttggggc	ccggctgggc	caagggtctg	ggcccatcca	cctgagtgag	gtgcgctgca	1260
59	ggggatatga	gcggaccctc	agcgactgcc	ctgccctgga	aggggtcccag	aatggttgcc	1320

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60 aacatgagaa tgctgctgct gtcagggtgca atgtccctaa catgggcttt cagaatcagg 1380
61 tgcgcttggc tgggtgggctg atccctgagg aggggctatt ggagggtgcag gtggagggtga 1440
62 acgggggtccc acgctggggg agcgtgtgca gtgaaaactg ggggctcacc gaagccatgg 1500
63 tggcctgccc acagctcggc ctgggttttg ccatccatgc ctacaaggaa acctggttct 1560
64 ggtcggggac gccaaaggcc caggagggtg tgatgagtgg ggtgcgctgc tcaggcacag 1620
65 agctggccct gcagcagtgc cagaggcagc ggccgggtgca ctgctcccac ggtggcgggc 1680
66 gcttctctggc tggagtctcc tgcattggaca gtgcaccaga cctgggtgat aacgcccagc 1740
67 tagtgacagga gacggcctac ttggaggacc gcccgctcag ccagctgtat tgtgcccacg 1800
68 aggagaactg cctctccaaag tctgcggatc acatggactg gccctacgga taccgcccgc 1860
69 tattgcgctt ctccacacag atctacaatc tggggccggac tgactttcgt ccaaagactg 1920
70 gacgcgatag ctgggttttg caccagtgc acaggcatta ccacagcatt gaggtcttca 1980
71 cccactacga cctctcact ctcaatggct ccaagggtggc tgaggggac aaggccagct 2040
72 tctgtctgga ggacacaaac tgccccacag gactgcagcg gcgctacgca tgtgccaact 2100
73 ttggagaaca gggagtgaat gtaggtctgt gggacacctc ccggcatgac attgattgcc 2160
74 agtgggtgga tatcacagat gtgggccccg ggaattatat cttccagggtg attgtgaacc 2220
75 cccactatga agtggcagag tcagatttct ccaacaatat gctgcagtgc cgtgcaagt 2280
76 atgatgggca ccgggtctgg ctgcacaact gccacacagg gaattcatac ccagccaatg 2340
77 cagaactctc cctggagcag gaacagcgct tcaggaaaca cctcatctga agctgtcact 2400
78 gcacactcct agctgtctgc gatacacca atacctcagc ttattggagc catgcccctc 2460
79 acagagtcct aactcagagg aaaaggggca gtgccaaggg gcaccaagaa cctgctcagg 2520
80 aagccttttg atggcaagat caccaatcca gatggtattg ctccctcagg atggtcttgg 2580
81 gcctgcccct aagggcctgt ggcctatgga atatgtctc caggctttgc tcagctgagc 2640
82 tctctctctg taaggaaacc cagtcctccc tgaatcttgc cacagagatc cgggattcag 2700
83 gagctctcag tttcttaggg atggactatg gccagctccc ccattctaagt ggtgctttgc 2760
84 aaatgtcttg gaggagtata ggacagagga ccaaaatata cagcaggtag tgttagctct 2820
85 ctgctaggag ctcaaagcaa cacaacttgt atcaaaatca caactggcag agaagctggt 2880
86 ggatccaatc ctttcttcat ctgttggtat ttagaactca cctctcacac tctgttcttt 2940
87 agtgtcctta cctttatctt accacacaca tgggtgtttc tattatcctt ggaagcacag 3000
88 acctcgggca tccccttatt gctgatggg ccaacaccaa cagttacgga gtgcttgaga 3060
89 aggggcaagt ttcacagaaa tggccagata gggccttctt acagagcagc aagagtaggc 3120
90 caagcagaaa gactgtgag gtaacacgga cccagcccc tgtcaggggc tctgccaagg 3180
91 aaataatatg gaccatttac ctggcaggca gtctgtctc tctcaggatc accacgcatt 3240
92 tcaggatttg tctaaacttc aagtctcaac caagtgtctg aagtgaactt tgcattgaat 3300
93 aaatttttgc catggaagaa acatcaaaac agccactcat ctctacagag ataagaaaac 3360
94 aagtttggca gagcaagaga cagaagaccg tggagaaatc agaaggggga acagtcagtt 3420
95 tagttaagga tggaaacctg gaaaggccac cattcctgct tgatggggct ctgatttgc 3480
96 cttgctcaag tggaaataaaa ccccatggtc ttcttgacat gattcttgat cttttctcca 3540
97 ctgagacaca cttaagtgat gatccttaca ggactgacac cctaattgca ataaaagttg 3600
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100 <210> SEQ ID NO: 2

101 <211> LENGTH: 756

102 <212> TYPE: PRT

103 <213> ORGANISM: Human

105 <400> SEQUENCE: 2

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106 Met Ala Trp Ser Pro Pro Ala Thr Leu Phe Leu Phe Leu Leu Leu
107   1           5           10           15
108 Gly Gln Pro Pro Ser Arg Pro Gln Ser Leu Gly Thr Thr Lys Leu
109           20           25           30
110 Arg Leu Val Gly Pro Glu Ser Lys Pro Glu Glu Gly Arg Leu Glu Val

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160 Leu Leu Glu Val Gln Val Glu Val Asn Gly Val Pro Arg Trp Gly Ser
161           435                      440                      445
162 Val Cys Ser Glu Asn Trp Gly Leu Thr Glu Ala Met Val Ala Cys Arg
163           450                      455                      460
164 Gln Leu Gly Leu Gly Phe Ala Ile His Ala Tyr Lys Glu Thr Trp Phe
165 465                      470                      475                      480
166 Trp Ser Gly Thr Pro Arg Ala Gln Glu Val Val Met Ser Gly Val Arg
167           485                      490                      495
168 Cys Ser Gly Thr Glu Leu Ala Leu Gln Gln Cys Gln Arg His Gly Pro
169           500                      505                      510
170 Val His Cys Ser His Gly Gly Gly Arg Phe Leu Ala Gly Val Ser Cys
171           515                      520                      525
172 Met Asp Ser Ala Pro Asp Leu Val Met Asn Ala Gln Leu Val Gln Glu
173           530                      535                      540
174 Thr Ala Tyr Leu Glu Asp Arg Pro Leu Ser Gln Leu Tyr Cys Ala His
175 545                      550                      555                      560
176 Glu Glu Asn Cys Leu Ser Lys Ser Ala Asp His Met Asp Trp Pro Tyr
177           565                      570                      575
178 Gly Tyr Arg Arg Leu Leu Arg Phe Ser Thr Gln Ile Tyr Asn Leu Gly
179           580                      585                      590
180 Arg Thr Asp Phe Arg Pro Lys Thr Gly Arg Asp Ser Trp Val Trp His
181           595                      600                      605
182 Gln Cys His Arg His Tyr His Ser Ile Glu Val Phe Thr His Tyr Asp
183 610                      615                      620
184 Leu Leu Thr Leu Asn Gly Ser Lys Val Ala Glu Gly His Lys Ala Ser
185 625                      630                      635                      640
186 Phe Cys Leu Glu Asp Thr Asn Cys Pro Thr Gly Leu Gln Arg Arg Tyr
187           645                      650                      655
188 Ala Cys Ala Asn Phe Gly Glu Gln Gly Val Thr Val Gly Cys Trp Asp
189           660                      665                      670
190 Thr Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val
191 675                      680                      685
192 Gly Pro Gly Asn Tyr Ile Phe Gln Val Ile Val Asn Pro His Tyr Glu
193 690                      695                      700
194 Val Ala Glu Ser Asp Phe Ser Asn Asn Met Leu Gln Cys Arg Cys Lys
195 705                      710                      715                      720
196 Tyr Asp Gly His Arg Val Trp Leu His Asn Cys His Thr Gly Asn Ser
197           725                      730                      735
198 Tyr Pro Ala Asn Ala Glu Leu Ser Leu Glu Gln Glu Gln Arg Leu Arg
199           740                      745                      750
200 Asn Asn Leu Ile
201           755
203 <210> SEQ ID NO: 3
204 <211> LENGTH: 103 ✓
205 <212> TYPE: PRT
206 <213> ORGANISM: Human
208 <400> SEQUENCE: 3
209 Leu Arg Leu Val Glu Pro Glu Ser Lys Pro Glu Glu Gly Arg Leu Glu
210 1                      5                      10                      15

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DATE: 08/16/2001

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Input Set : A:\Seqlist.txt

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211 Val Leu His Gln Gly Gln Trp Gly Thr Val Cys Asp Asp Asn Phe Ala
212          20          25          30
213 Ile Gln Glu Ala Thr Val Ala Cys Arg Gln Leu Gly Phe Glu Ala Ala
214          35          40          45
215 Leu Thr Trp Ala His Ser Ala Lys Tyr Gly Gln Gly Glu Gly Pro Ile
216          50          55          60
217 Trp Leu Asp Asn Val Arg Cys Val Gly Thr Glu Ser Ser Leu Asp Gln
218          65          70          75          80
219 Cys Gly Ser Asn Gly Trp Gly Val Ser Asp Cys Ser His Ser Glu Asp
220          85          90          95
221 Val Gly Val Ile Cys His Pro
222          100
224 <210> SEQ ID NO: 4
225 <211> LENGTH: 125
226 <212> TYPE: PRT
227 <213> ORGANISM: Human
229 <400> SEQUENCE: 4
230 Pro Ile Leu Ala Ser Ala Lys Gln His Ser Pro Val Thr Glu Gly Ala
231 1          5          10          15
232 Val Glu Val Lys Tyr Glu Gly His Trp Arg Gln Val Cys Asp Gln Gly
233          20          25          30
234 Trp Thr Met Asn Asn Ser Arg Val Val Cys Gly Met Leu Gly Phe Pro
235          35          40          45
236 Ser Glu Val Pro Val Asp Ser His Tyr Tyr Arg Lys Val Trp Asp Leu
237          50          55          60
238 Lys Met Arg Asp Pro Lys Ser Arg Leu Lys Ser Leu Thr Asn Lys Asn
239          65          70          75          80
240 Ser Phe Trp Ile His Gln Val Thr Cys Leu Gly Thr Glu Pro His Met
241          85          90          95
242 Ala Asn Cys Gln Val Gln Val Ala Pro Ala Arg Gly Lys Leu Arg Pro
243          100          105          110
244 Ala Cys Pro Gly Gly Met His Ala Val Val Ser Cys Val
245          115          120          125
247 <210> SEQ ID NO: 5
248 <211> LENGTH: 101
249 <212> TYPE: PRT
250 <213> ORGANISM: Human
252 <400> SEQUENCE: 5
253 Val Arg Leu Arg Ser Gly Ala Gln Val Gly Glu Gly Arg Val Glu Val
254 1          5          10          15
255 Leu Met Asn Arg Gln Trp Gly Thr Val Cys Asp His Arg Trp Asn Leu
256          20          25          30
257 Ile Ser Ala Ser Val Val Cys Arg Gln Leu Gly Phe Gly Ser Ala Arg
258          35          40          45
259 Glu Ala Leu Phe Gly Ala Arg Leu Gly Gln Gly Leu Gly Pro Ile His
260          50          55          60
261 Leu Ser Glu Val Arg Cys Arg Gly Tyr Glu Arg Thr Leu Ser Asp Cys
262          65          70          75          80
263 Pro Ala Leu Glu Gly Ser Gln Asn Gly Cys Gln His Glu Asn Ala Ala

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/924,946

DATE: 08/16/2001

TIME: 12:48:59

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\08162001\I924946.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:329 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:340 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:351 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:362 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11

checked OK